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Patent

Attorney Docket No. 54318.8001.US01
#8
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11-27-02

CERTIFICATE OF MAILING

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Date: November 18, 2002By: Miguel J. Paez

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE APPLICATION OF: DEBE, Derek A. *et al.*

APPLICATION No.: 09/905,176

FILED: July 12, 2001

FOR: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM PRIMARY PROTEIN SEQUENCE

EXAMINER: BORIN, MICHAEL

ART UNIT: 1631

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INFORMATION DISCLOSURE STATEMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

In accordance with 37 CFR §§ 1.97 and 1.98, the items identified in this Information Disclosure Statement (“IDS”) are brought to the attention of the Office. The items are listed on the attached Form PTO-1449 and copies are enclosed for the convenience of the Examiner.

The items identified in this IDS may or may not be “material” pursuant to 37 CFR § 1.56. The submission thereof by Applicant is not to be construed as an admission that any such patent, publication or other information referred to therein is material or considered to be material (37 CFR § 1.97(h)), or even qualifies as “prior art” under 35 USC § 102 with respect to this invention unless specifically designated by Applicant as such.

INFORMATION DISCLOSURE STATEMENT FILING PROVISION:

This IDS is believed to be timely in that it is being submitted under 37 CFR § 1.97(b), that is (1) within three months of the filing date of the application, which is not a continued prosecution application filed under § 1.53(d); or (2) within three months of entry of the national stage as set forth in 37 CFR § 1.491; or (3) before the mailing of a first Office action on the merits; or (4) before the

mailing of a first Office action after filing a request for continued examination under § 1.114. Thus, no fee is required.

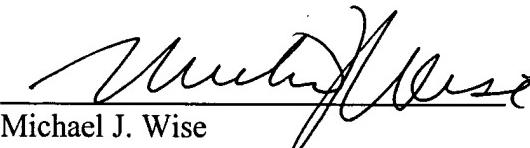
However, if the undersigned is in error in this regard, Applicant respectfully requests that the Office consider this IDS as filed under 37 CFR § 1.97(c), if applicable, and charge the fee due under 37 CFR §1.17(p) to the deposit account referenced below.

The Commissioner is authorized to charge any fees required by the filing of these papers, and to credit any overpayment to Deposit Account No. **50-0665**.

Respectfully submitted,
Perkins Coie LLP

Dated: 11/18/02

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ATTY. DOCKET NO.
54318.8001.US0SERIAL NO.
09/905,176LIST OF PATENTS AND OTHER ITEMS FOR APPLICANT'S
INFORMATION DISCLOSURE STATEMENTAPPLICANT:
DEBE, Derek A.FILING DATE:
July 12, 2001GROUP:
1645

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U.S. PATENT DOCUMENTS

EXAMINE R INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
AA						
AB						
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FOREIGN PATENT DOCUMENTS

EXAMINE R INITIAL	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	TRANSLATIO YES	NO
AI							
AJ							
AK							

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, etc.)

AL	Altschul, F., et al., "Basic Local Alignment Search Tool", J. Mol. Biol., Vol. 215 (1990), pp. 403-410
AM	Altschul, F., et al., "Gapped BLAST and PSI-BLAST: A new generation of protein database search programs", Nuc. Acids Res., Vol. 25, No. 17 (1997), pp. 3389-3402
AN	Aszódi, A., et al. "Homology modelling by distance geometry", Folding & Design Struct., Vol. 1 (1996), pp. 325-334
AO	Berman, H., et al., "The Protein Data Bank", Nuc. Acids Res., Vol. 28, No. 1 (2000), pp. 235-242
AP	Bernstein, F.C., et al., "The Protein Data Bank: A Computer-based Archival File for Macromolecular Structures", J. Mol. Biol., Vol. 112 (1977), pp. 535-542
AQ	Blundell, T.L., et al., "Knowledge-based prediction of protein structures and the design of novel molecules", Nature, Vol. 326 (1987), pp. 347-352
AR	Bowie, J., et al., "A Method to Identify Protein Sequences That Fold into a Known Three-Dimensional Structure", Science, Vol. 253 (1991), pp. 164-170

[54318-8001/LA023020.075]

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DATE CONSIDERED:

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LIST OF PATENTS AND OTHER ITEMS FOR APPLICANT'S
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(Use several sheets if necessary)

APPLICANT:
DEBE, Derek A.

FILING DATE: July 12, 2001 GROUP: 1645

NOV 21 2002 PATENT & TRADEMARK OFFICE JC 26 AS	Brenner, S., et al., "Population statistics of protein structures: lessons from structural classifications", Current Opinions on Structural Biology, Vol. 7 (1997), pp. 369-376
AT	Brocklehurst, S., et al., "Prediction of the three-dimensional structures of the biotinylated domain from yeast pyruvate carboxylase and of the lipoylated H-protein from the pea leaf glycine cleavage system: A new automated method for prediction of protein tertiary structure", Protein Science, Vol. 2 (1993), 626-639
AU	Browne, W.J., et al., "A Possible Three-dimensional Structure of Bovine α -Lactalbumin based on that of Hen's Egg-White Lysozyme", J. Mol. Biol., Vol. 42 (1969), pp. 65-86
AV	Burley, S., et al., "Structural genomics: beyond the Human Genome Project", Nature Gen., Vol. 23 (1999), pp. 151-157
AW	Classens, M., et al., "Modelling the polypeptide backbone with 'spare parts' from known protein structures", Prot. Eng., Vol. 2, No. 5 (1989), pp. 335-345
AX	Dayhoff, M.O., et al., "A Model of Evolutionary Change in Proteins", Atlas of Prot. Seq. & Struct., Vol. 5, Supp. 3 (1979), pp. 345-352
AY	Fischer, D., et al., "Protein fold recognition using sequence-derived predictions", Prot. Science, Vol. 5 (1996), pp. 947-955
AZ	Gibrat, J., et al., "Surprising similarities in structure comparison", Current Opinions on Structural Biology, Vol. 7 (1996), pp. 377-385
BA	Gotoh, O., "An Improved Algorithm for Matching Biological Sequences", J. Mol. Biol., Vol. 162 (1982), pp. 705-708
BB	Greer, J., "Comparative Modeling Methods: Application to the Family of the Mammalian Serine Proteases", Proteins: Structure, Function & Genetics, Vol. 7 (1990), pp. 317-334
BC	Gribskov, M., et al., "Profile Analysis", Methods of Enzymology, Vol. 183 (1990), pp. 146-159
BD	Gribskov, M., et al., "Profile analysis: Detection of distantly related proteins", Proc. Natl. Acad. Sci. USA, Vol. 84 (1987), pp. 4355-4358
BE	Gribskov, M., et al., "Detection of Protein Structural Features with Profile Analysis", Techniques In Protein Chemistry (1989), pp. 108-117
BF	Havel, T.F., et al., "A New Method for Building Protein Conformations from Sequence Alignments with Homologues of Known Structure", J. Mol. Biol., Vol. 217 (1991), pp. 1-7
BG	Heinkoff, S., et al., "Amino acid substitution matrices from protein blocks", Proc. Natl. Acad. Sci. USA, Vol. 89 (1992), pp. 10915-10919
BH	Holm, L., et al., "Protein Structure Comparison by Alignment of Distance Matrices", J. Mol. Biol., Vol. 233 (1993), pp. 123-138
BI	Holm, L., et al., "Mapping the Protein Universe", Science, Vol. 273, No. 5275 (1996), pp. 595-602
BJ	Jones, T.A., et al., "Using known substructures in protein model building and crystallography", EMBO J., Vol. 5, No. (1986), pp. 819-822
BK	Karplus, K., et al., "Hidden Markov models for detecting remote protein homologies", Bioinformatics, Vol. 14, No. 10 (1998), pp. 846-856
BL	Levitt, M. "Accurate Modeling of Protein Conformation by Automatic Segment Matching", J. Mol. Biol., Vol. 226 (1992), pp. 507-533
BM	Landahl, E., et al., "Identification of Related Proteins on Family, Superfamily and Fold Level", J. Mol. Biol., Vol. 295 (2000), pp. 613-625
BN	Murzin, A., et al., "SCOP: A Structural Classification of Proteins Database for the Investigation of Sequences and Structures", J. Mol. Biol., Vol. 247 (1995), pp. 536-540

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DEBE, Derek A.

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O I P E PATENT & TRADEMARK OFFICE NOV 21 2002 RECEIVED BP		Needleman, S., et al., "A General Method Applicable to the Search for Similarities in the Amino Acid Sequence of Two Proteins", <i>J. Mol. Biol.</i> , Vol. 48 (1970), pp. 443-453
BQ		Rost, B., et al., "Protein Fold Recognition by Prediction-based Threading", <i>J. Mol. Biol.</i> , Vol. 270 (1997), pp. 471-480
BQ		Sali, A., et al., "Comparative Protein Modelling by Satisfaction of Spatial Restraints", <i>J. Mol. Biol.</i> , Vol. 234 (1993), pp. 779-815
BR		Sánchez, R., et al., "ModBase: A database of comparative protein structure models", <i>Bioinformatics</i> , Vol. 15, No. 12 (1989), pp. 1060-1061
BS		Sánchez, R., et al., "Large-scale protein structure modeling of the <i>Saccharomyces cerevisiae</i> genome", <i>Proc. Natl. Acad. Sci. USA</i> , Vol. 95 (1998), pp. 13597-13602
BT		Shindyalov, I., et al., "Protein structure alignment by incremental combinatorial extension (CE) of the optimal path", <i>Prot. Eng.</i> , Vol. 11 (1998), pp. 739-747
BU		Sippl, M.J., "Recognition of Errors in Three-Dimensional Structures of Proteins", <i>Proteins: Struct, Function and Genetics</i> , Vol. 17 (1993), pp. 355-362
BV		Smith, T., et al., "Comparison of Biosequences", <i>Advances in Applied Math.</i> , Vol. 2, No. 4 (1981), pp. 482-489
BW		Smith, T., et al., "Identification of Common Molecular Subsequences", <i>J. Mol. Biol.</i> , Vol. 147 (1981), pp. 195-197
BX		Srinivasan, N., et al., "An evaluation of the performance of an automated procedure for comparative modeling of protein tertiary structure", <i>Prot. Eng.</i> , Vol. 6, No. 5 (1993), pp. 501-512
BY		Teichmann, S., et al., "Advances in structural genomics", <i>Current Opinions on Structural Biology</i> , Vol. 9 (1999), pp. 390-399
BZ		Thompson, J.D., et al., "CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice", <i>Nuc. Acids Res.</i> , Vol. 22, No. 22 (1994), pp. 4673-4680
CA		Unger, R., et al., "A 3D Building Blocks Approach to Analyzing and Predicting Structure of Proteins", <i>Proteins: Structure, Function, and Genetics</i> , Vol. 5 (1989), pp. 355-373
CB		Van Holde, K.E., "Fundamentals of X-Ray Diffraction", <i>X-Ray Diffraction</i> , 11 (1971), pp. 221-239
CC		Waterman, M.S., et al., "A New Algorithm for Best Subsequence Alignments with Application to tRNA-rRNA Comparisons", <i>J. Mol. Biol.</i> , Vol. 197 (1987), pp. 723-728

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